The Use of Multiple "Omic" Platforms to Evaluate the Effects of Endocrine Disrupting Compounds in Small Fish Species

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Linking molecular changes at multiple levels of biological organization using "omic" methods provides highly complimentary, "data-dense" information for predicting outcomes for organisms exposed to environmental contaminants. However, performing separate "omic" analyses on multiple organisms or tissues increases the variability in responses and the uncertainty of the linkages between these levels of organization. Ideally, performing transcriptomic, proteomic, and metabolomic analyses on the same sample of individual tissues of interest from an organism would reduce this uncertainty and biological variation. On-going research in our laboratory has demonstrated the ability to apply multiple "omic" technologies to analyze individual tissues of small fish species. In the present study, transcriptomic and proteomic analyses were performed on hepatic tissues from individual adult female fathead minnows (FHM; *Pimephales promelas*) exposed to the aromatase inhibitor fadrozole. Organisms were exposed to 0, 0.04, and 1.0 µg/L fadrozole for 4 days and tissue extracts were analyzed using an LC-MS/MS based, label-free proteomics approach that identified over 1000 proteins. Many of the differentially-expressed proteins in fadrozole-exposed female livers were consistent with published results for fadrozole. Interpretation of the broader proteomic response will be discussed in the context of transcriptomic data collected using mRNA isolated from the same samples used in proteomic analyses. Our data demonstrates the ability to extract high quality RNA and protein samples from small quantities (10 mg) of single tissues for comprehensive 'omic' analyses. Overall, our ability to perform multiple "omic" analyses on individual tissues of small fish species provides greatly improved information for connecting various levels of biological organization and elucidating pathways of toxicity. This information provides a more comprehensive representation of the "systems effects" resulting from chemical exposures and will ideally serve as a basis for advancements in predictive ecotoxicology.

STICs Field	Entry
1 – Influence/profile	Not applicable
2 – Clearance tracking no.	Assigned automatically
3 – Principal Investigator / Project Officer	Kim Ralston-Hooper Lead EPA Contact – Dan Villeneuve
4- Product title	Copy and paste from abstract
5 - Authors	See abstract
6a- Product type	Presentations and technical summaries
6b-Product subtype	Abstract
6c – Records schedule	Not a senior official
7a – Impact statement	n/a
7b- Product description	Paste in abstract
8 – Bibliographic citation	SETAC North America 33rd Annual Meeting, 11-15 November, Long Beach, CA, USA.
9 - Access	Public
10 – Tracking and Planning Task	2.1.1 2.1.1: Adverse outcome pathway (AOP) discovery and definition
10 – Tracking and Planning Product	(2) AOP descriptions comparing linkages (e.g., causal) between specific pathway perturbations and reproductive or developmental outcomes in multiple species (e.g., rodents, fish, invertebrates) (reports). These will provide data that support the development of tools and guidance cross-species extrapolation of effects and hazard.
11 – Copyright permission	No
12 - QA	not applicable
13 – Policy implications	No
14 - Keywords	transcriptomics proteomics metabolomics steroidogenesis

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